

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys
1				5					10					15	

Pro Ala

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe
 1 5 10 15

Asp Ala Cys Gly Phe
 20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly
 1 5 10 15

Tyr Ser Thr Ser Leu
 20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His
 1 5 10 15
 Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu
 20 25 30
 Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln
 35 40 45
 Asp Ser
 50

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val
 1 5 10 15
 Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr
 20 25 30
 Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr
 35 40 45
 Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met
 1 5 10 15
 Val Asn Phe Val Leu Phe Ile Gly Ile Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser
 1 5 10 15
 Ser Ile Tyr

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Arg Leu Ala Arg Ser Thr Leu Leu Ile Pro Leu Phe Gly Ile
 1 5 10 15

His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu
 20 25 30
 Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val
 35 40 45
 Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys
 50 55 60
 Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe
 65 70 75

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly
 1 5 10 15
 Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met
 20 25 30
 Ser

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
 1 5 10 15
 Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp
 20 25

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	1	5	10	15
Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp	Ser	Ser	Pro	20	25	30	
Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His	35	40	45	
Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	Phe	50	55	60	
Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Phe	Gly	Phe	65	70	75	80
Ala	Asp	Ser	Lys	Ser	Leu	Asp	Leu	Ser	Asp	Met	Arg	Val	Val	Ser	Arg	85	90	95	
Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	100	105	110	
Ala	Cys	Gly	Phe	Glu	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	115	120	125	
Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	130	135	140	
Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	145	150	155	160
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	165	170	175	
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	180	185	190	
Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala	195	200	205	

Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu
210 215 220

Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe
225 230 235 240

Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile Ile Gly Trp Gly Thr
245 250 255

Pro Thr Val Cys Val Ser Val Trp Ala Met Leu Arg Leu Tyr Phe Asp
260 265 270

Asp Thr Gly Cys Trp Asp Met Asn Asp Asn Thr Ala Leu Trp Trp Val
275 280 285

Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe
290 295 300

Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met
305 310 315 320

Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr
325 330 335

Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu
340 345 350

Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro
355 360 365

Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val
370 375 380

Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln
385 390 395 400

Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln
405 410 415

Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe
420 425 430

Thr Met Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val
435 440 445

Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile
450 455 460

Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
465 470 475

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Arg	Gly	Gly	Arg	His	Trp	Pro	Glu	Pro	Pro	Cys	Arg	Leu	Arg	Ser	1	5	10	15
Val	Met	Ala	Ser	Ile	Ala	Gln	Val	Ser	Leu	Ala	Ala	Leu	Leu	Leu	Leu	20	25	30	
Pro	Met	Ala	Thr	Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	35	40	45	
Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	50	55	60	
Asn	Asp	Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	65	70	75	80
Trp	Lys	Pro	Ala	His	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	85	90	95	
Leu	Phe	Arg	Ile	Phe	Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	100	105	110	
Gly	Glu	Phe	Gly	Phe	Ala	Asp	Ser	Lys	Ser	Leu	Asp	Leu	Ser	Asp	Met	115	120	125	
Arg	Val	Val	Ser	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	130	135	140	
Pro	His	Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Glu	Glu	Tyr	Glu	Ser	Glu	Thr	145	150	155	160
Gly	Asp	Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	165	170	175	
Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	180	185	190	
Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	195	200	205	
Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	210	215	220	

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Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr
225 230 235 240

Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser
245 250 255

Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu
260 265 270

Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile
275 280 285

Ile Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu
290 295 300

Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Asn Thr
305 310 315 320

Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val
325 330 335

Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu
340 345 350

Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys
355 360 365

Val	Gln	Lys	Cys	Tyr	Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys
370						375					380				

Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr
385 390 395 400

Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe
405 410 415

Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly
420 425 430

Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu
435 440 445

Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys
450 455 460

Val	Asn	Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu
465					470					475					480

Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys
485 490 495

Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala

500

505

510

Thr

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	1	5	10	15
Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp	Ser	Ser	Pro	20	25	30	
Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His	35	40	45	
Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	Phe	50	55	60	
Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Phe	Gly	Phe	65	70	75	80
Ala	Asp	Ser	Lys	Ser	Leu	Asp	Leu	Ser	Asp	Met	Arg	Val	Val	Ser	Arg	85	90	95	
Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	100	105	110	
Ala	Cys	Gly	Phe	Glu	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	115	120	125	
Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	130	135	140	
Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	145	150	155	160
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	165	170	175	
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala				

180					185					190					
Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala
		195					200					205			
Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu
	210					215					220				
Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe
225					230					235					240
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Ile	Ile	Ile	Gly	Trp	Gly	Thr
				245					250					255	
Pro	Thr	Val	Cys	Val	Ser	Val	Trp	Ala	Met	Leu	Arg	Leu	Tyr	Phe	Asp
			260					265					270		
Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Asn	Thr	Ala	Leu	Trp	Trp	Val
		275					280					285			
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe
	290					295					300				
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met
305					310					315					320
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
				325					330					335	
Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser
			340					345					350		
Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu
		355					360					365			
Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn
	370					375					380				
Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val
385					390					395					400
Asn	Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala
				405					410					415	
Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser
			420					425					430		
Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr
		435					440					445			

(A) LENGTH: 485 amino acids

(D) TOPOLOGY: linear

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp
210 215 220

Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Val	Ser	Thr	225	230	235	240
Val	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	245	250	255	
Asn	Tyr	Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	260	265	270	
Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Ile	Ile	275	280	285	
Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Ser	Val	Trp	Ala	Met	Leu	290	295	300	
Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Asn	Thr	305	310	315	320
Ala	Leu	Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	325	330	335	
Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	340	345	350	
Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Arg	Leu	355	360	365	
Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	370	375	380	
Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	385	390	395	400
Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	405	410	415	
Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	420	425	430	
Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	His	Arg	435	440	445	
His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	450	455	460	
Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	465	470	475	480
Asp	Asn	Leu	Ala	Thr	485														

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	1	5	10	15
Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu	Ser	Ser	Pro	20	25	30	
Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	Gln	35	40	45	
Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Val	Phe	Arg	Ile	Phe	50	55	60	
Asn	Pro	Asp	Gln	Val	Trp	Met	Thr	Glu	Thr	Ile	Gly	Asp	Ser	Gly	Phe	65	70	75	80
Ala	Asp	Ser	Asn	Ser	Leu	Glu	Ile	Thr	Asp	Met	Gly	Val	Val	Gly	Arg	85	90	95	
Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	100	105	110	
Ala	Cys	Gly	Phe	Asp	Asp	Tyr	Glu	Pro	Glu	Ser	Gly	Asp	Gln	Asp	Tyr	115	120	125	
Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	130	135	140	
Leu	Ala	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	145	150	155	160
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	165	170	175	
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	180	185	190	
Glu	Gln	Asp	Ser	Ser	His	Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala	195	200	205	
Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu	210	215	220	

Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	225	230	235	240
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr	245	250	255	
Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Val	Leu	Arg	Leu	Tyr	Phe	Asp	260	265	270	
Asp	Ala	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val	275	280	285	
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	290	295	300	
Ile	Gly	Ile	Ile	Ile	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	305	310	315	320
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	325	330	335	
Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	340	345	350	
Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	355	360	365	
Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	370	375	380	
Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	385	390	395	400
Asn	Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	405	410	415	
Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	420	425	430	
Ser	Ser	Gln	Leu	Arg	Met	Ser	Ser	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr	435	440	445	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Ala	Arg	Val	Leu	Gln	Leu	Ser	Leu	Thr	Ala	Leu	Leu	Leu	Pro	Val	1	5	10	15
Ala	Ile	Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	20	25	30	
Cys	Leu	Glu	Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu	35	40	45	
Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	50	55	60	
Pro	Ala	Gln	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Val	Phe	65	70	75	80
Arg	Ile	Phe	Asn	Pro	Asp	Gln	Val	Trp	Met	Thr	Glu	Thr	Ile	Gly	Asp	85	90	95	
Ser	Gly	Phe	Ala	Asp	Ser	Asn	Ser	Leu	Glu	Ile	Thr	Asp	Met	Gly	Val	100	105	110	
Val	Gly	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	115	120	125	
Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Asp	Asp	Tyr	Glu	Pro	Glu	Ser	Gly	Asp	130	135	140	
Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	145	150	155	160
Ser	Thr	Ser	Leu	Ala	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	165	170	175	
Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	180	185	190	
Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	195	200	205	
Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Ser	His	Cys	Phe	Val	Ser	Thr	Val	Glu	210	215	220	
Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	225	230	235	240
Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	245	250	255	
Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly				

260					265					270					
Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Val	Leu	Arg	Leu
		275					280					285			
Tyr	Phe	Asp	Asp	Ala	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu
	290					295					300				
Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe
305					310					315					320
Val	Leu	Phe	Ile	Gly	Ile	Ile	Ile	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser
				325					330					335	
Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Arg	Leu	Ala	Arg
			340					345					350		
Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe
		355					360					365			
Ala	Phe	Ser	Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu
	370					375					380				
Leu	Gly	Leu	Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys
385					390					395					400
Phe	Leu	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser
				405					410					415	
Trp	Lys	Val	Asn	Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro
			420					425					430		
Ser	Leu	Ala	Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu
		435					440					445			
Ser	Lys	Ser	Ser	Ser	Gln	Leu	Arg	Met	Ser	Ser	Leu	Pro	Ala	Asp	Asn
	450					455					460				
Leu	Ala	Thr													
465															

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	1	5	10	15
Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu	Ser	Ser	Pro	20	25	30	
Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	Gln	35	40	45	
Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Val	Phe	Arg	Ile	Phe	50	55	60	
Asn	Pro	Asp	Gln	Val	Trp	Met	Thr	Glu	Thr	Ile	Gly	Asp	Ser	Gly	Phe	65	70	75	80
Ala	Asp	Ser	Asn	Ser	Leu	Glu	Ile	Thr	Asp	Met	Gly	Val	Val	Gly	Arg	85	90	95	
Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	100	105	110	
Ala	Cys	Gly	Phe	Asp	Asp	Tyr	Glu	Pro	Glu	Ser	Gly	Asp	Gln	Asp	Tyr	115	120	125	
Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	130	135	140	
Leu	Ala	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	145	150	155	160
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	165	170	175	
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	180	185	190	
Glu	Gln	Asp	Ser	Ser	His	Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala	195	200	205	
Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu	210	215	220	
Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	225	230	235	240
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr	245	250	255	
Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Val	Leu	Arg	Leu	Tyr	Phe	Asp	260	265	270	

Asp	Ala	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val
		275					280					285			
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe
	290					295					300				
Ile	Gly	Ile	Ile	Ile	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met
305					310					315					320
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr
			325						330					335	
Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu
			340					345					350		
Ser	Thr	Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro
		355					360					365			
Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val
	370					375					380				
Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln
385					390					395					400
Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln
				405					410					415	
Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe
			420					425					430		
Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val
		435					440					445			
Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Leu
	450					455					460				
Arg	Met	Ser	Ser	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr				
465					470					475					

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Ala	Arg	Val	Leu	Gln	Leu	Ser	Leu	Thr	Ala	Leu	Leu	Leu	Pro	Val	1	5	10	15
Ala	Ile	Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	20	25	30	
Cys	Leu	Glu	Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu	35	40	45	
Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	50	55	60	
Pro	Ala	Gln	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Val	Phe	65	70	75	80
Arg	Ile	Phe	Asn	Pro	Asp	Gln	Val	Trp	Met	Thr	Glu	Thr	Ile	Gly	Asp	85	90		95
Ser	Gly	Phe	Ala	Asp	Ser	Asn	Ser	Leu	Glu	Ile	Thr	Asp	Met	Gly	Val	100	105		110
Val	Gly	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	115	120		125
Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Asp	Asp	Tyr	Glu	Pro	Glu	Ser	Gly	Asp	130	135		140
Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	145	150	155	160
Ser	Thr	Ser	Leu	Ala	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	165	170		175
Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	180	185		190
Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	195	200		205
Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Ser	His	Cys	Phe	Val	Ser	Thr	Val	Glu	210	215		220
Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	225	230	235	240
Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	245	250		255
Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	260	265		270
Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Val	Leu	Arg	Leu				

275					280					285					
Tyr	Phe	Asp	Asp	Ala	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu
	290					295					300				
Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe
305					310					315					320
Val	Leu	Phe	Ile	Gly	Ile	Ile	Ile	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser
				325					330					335	
Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln
			340					345					350		
Lys	Cys	Tyr	Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met
		355					360					365			
Ser	Glu	Leu	Ser	Thr	Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu
	370					375					380				
Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro
385					390					395					400
Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly
				405					410					415	
Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly
			420					425					430		
Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn
		435					440					445			
Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser
	450					455					460				
Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser
465					470					475					480
Ser	Gln	Leu	Arg	Met	Ser	Ser	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr	
				485					490					495	

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Met 1	His	Ser	Asp	Cys 5	Ile	Phe	Lys	Lys	Glu 10	Gln	Ala	Met	Cys	Leu 15	Glu
Lys	Ile	Gln	Arg 20	Ala	Asn	Glu	Leu	Met 25	Gly	Phe	Asn	Asp	Ser 30	Ser	Pro
Gly	Cys	Pro 35	Gly	Met	Trp	Asp	Asn 40	Ile	Thr	Cys	Trp	Lys 45	Pro	Ala	His
Val	Gly 50	Glu	Met	Val	Leu	Val 55	Ser	Cys	Pro	Glu	Leu 60	Phe	Arg	Ile	Phe
Asn 65	Pro	Asp	Gln	Val	Trp 70	Glu	Thr	Glu	Thr	Ile 75	Gly	Glu	Ser	Asp	Phe 80
Gly	Asp	Ser	Asn	Ser 85	Leu	Asp	Leu	Ser	Asp 90	Met	Gly	Val	Val	Ser	Arg
Asn	Cys	Thr	Glu 100	Asp	Gly	Trp	Ser	Glu 105	Pro	Phe	Pro	His	Tyr 110	Phe	Asp
Ala	Cys	Gly 115	Phe	Asp	Glu	Tyr	Glu 120	Ser	Glu	Thr	Gly	Asp 125	Gln	Asp	Tyr
Tyr 130	Tyr	Leu	Ser	Val	Lys	Ala 135	Leu	Tyr	Thr	Val	Gly 140	Tyr	Ser	Thr	Ser
Leu 145	Val	Thr	Leu	Thr	Thr 150	Ala	Met	Val	Ile	Leu 155	Cys	Arg	Phe	Arg	Lys 160
Leu	His	Cys	Thr	Arg 165	Asn	Phe	Ile	His	Met 170	Asn	Leu	Phe	Val	Ser	Phe 175
Met	Leu	Arg	Ala 180	Ile	Ser	Val	Phe	Ile 185	Lys	Asp	Trp	Ile	Leu 190	Tyr	Ala
Glu	Gln	Asp 195	Ser	Asn	His	Cys	Phe 200	Ile	Ser	Thr	Val	Glu 205	Cys	Lys	Ala
Val 210	Met	Val	Phe	Phe	His	Tyr 215	Cys	Val	Val	Ser	Asn 220	Tyr	Phe	Trp	Leu
Phe 225	Ile	Glu	Gly	Leu	Tyr 230	Leu	Phe	Thr	Leu 235	Leu	Val	Glu	Thr	Phe	Phe 240
Pro	Glu	Arg	Arg	Tyr 245	Phe	Tyr	Trp	Tyr	Thr 250	Ile	Ile	Gly	Trp	Gly 255	Thr
Pro	Thr	Val	Cys 260	Val	Thr	Val	Trp	Ala 265	Thr	Leu	Arg	Leu	Tyr 270	Phe	Asp

Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val
		275					280					285			
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe
	290					295					300				
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met
305					310					315				320	
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
				325					330					335	
Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser
			340					345					350		
Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu
		355					360					365			
Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn
	370					375					380				
Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val
385					390					395				400	
Asn	Arg	Tyr	Phe	Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala
			405						410					415	
Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser
			420					425					430		
Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr
		435					440					445			

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	Ala	His	Cys	Gly	Ala	Cys
1				5					10					15	
Pro	Trp	Gly	Arg	Gly	Arg	Leu	Arg	Lys	Gly	Arg	Ala	Ala	Cys	Lys	Ser
			20					25					30		

Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu Leu Ser Val Gly
35 40 45

Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val
50 55 60

Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser
65 70 75 80

Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln
85 90 95

Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro
100 105 110

Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu
115 120 125

Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp
130 135 140

Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser
145 150 155 160

Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr
165 170 175

Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly
180 185 190

Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu
195 200 205

Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr
210 215 220

Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys
225 230 235 240

Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg
245 250 255

Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp
260 265 270

Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val
275 280 285

Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu
290 295 300

Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg

305		310		315		320
Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val	325		330		335	
Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly	340		345		350	
Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile Lys Gly	355		360		365	
Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile	370		375		380	
Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn	385		390		395	400
Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile	405		410		415	
Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn	420		425		430	
Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe	435		440		445	
Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val	450		455		460	
Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr	465		470		475	480
Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly	485		490		495	
Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser-Gln	500		505		510	
Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr	515		520		525	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
1				5					10					15	
Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp	Ser	Ser	Pro
			20					25					30		
Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His
		35					40					45			
Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	Phe
	50					55					60				
Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Ser	Asp	Phe
65					70					75					80
Gly	Asp	Ser	Asn	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	Arg
				85					90					95	
Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp
			100					105					110		
Ala	Cys	Gly	Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr
		115					120					125			
Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser
	130					135					140				
Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys
145					150					155					160
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe
				165					170					175	
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala
			180					185					190		
Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys	Ala
		195					200					205			
Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu
	210					215					220				
Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe
225					230					235					240
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr
				245					250					255	
Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Thr	Leu	Arg	Leu	Tyr	Phe	Asp
			260					265					270		

Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val		
		275					280					285					
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe		
	290					295					300						
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met		
305					310					315					320		
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr		
			325						330					335			
Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu		
			340					345					350				
Ser	Thr	Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro		
		355					360					365					
Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val		
	370					375					380						
Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln		
385					390					395					400		
Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln		
				405					410					415			
Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe		
			420					425					430				
Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val		
		435					440					445					
Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile		
	450					455					460						
Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr						
465					470					475							

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met 1	Ala	Gly	Val 5	Val	His	Val	Ser	Leu 10	Ala	His	Cys	Gly	Ala 15	Cys	
Pro	Trp	Gly	Arg 20	Gly	Arg	Leu	Arg	Lys 25	Gly	Arg	Ala	Ala	Cys 30	Lys	Ser
Ala	Ala	Gln 35	Arg	His	Ile	Gly	Ala 40	Asp	Leu	Pro	Leu	Leu 45	Ser	Val	Gly
Gly	Gln 50	Trp	Cys	Trp	Pro	Arg 55	Ser	Val	Met	Ala	Gly 60	Val	Val	His	Val
Ser 65	Leu	Ala	Ala	Leu	Leu 70	Leu	Leu	Pro	Met	Ala 75	Pro	Ala	Met	His	Ser 80
Asp	Cys	Ile	Phe	Lys 85	Lys	Glu	Gln	Ala	Met 90	Cys	Leu	Glu	Lys	Ile 95	Gln
Arg	Ala	Asn	Glu 100	Leu	Met	Gly	Phe	Asn 105	Asp	Ser	Ser	Pro	Gly 110	Cys	Pro
Gly	Met	Trp 115	Asp	Asn	Ile	Thr	Cys 120	Trp	Lys	Pro	Ala	His 125	Val	Gly	Glu
Met	Val 130	Leu	Val	Ser	Cys	Pro 135	Glu	Leu	Phe	Arg	Ile 140	Phe	Asn	Pro	Asp
Gln 145	Val	Trp	Glu	Thr	Glu 150	Thr	Ile	Gly	Glu	Ser 155	Asp	Phe	Gly	Asp	Ser 160
Asn	Ser	Leu	Asp	Leu 165	Ser	Asp	Met	Gly	Val 170	Val	Ser	Arg	Asn	Cys 175	Thr
Glu	Asp	Gly	Trp 180	Ser	Glu	Pro	Phe	Pro 185	His	Tyr	Phe	Asp	Ala 190	Cys	Gly
Phe	Asp	Glu 195	Tyr	Glu	Ser	Glu	Thr 200	Gly	Asp	Gln	Asp	Tyr 205	Tyr	Tyr	Leu
Ser	Val 210	Lys	Ala	Leu	Tyr	Thr 215	Val	Gly	Tyr	Ser	Thr 220	Ser	Leu	Val	Thr
Leu 225	Thr	Thr	Ala	Met	Val 230	Ile	Leu	Cys	Arg	Phe 235	Arg	Lys	Leu	His	Cys 240
Thr	Arg	Asn	Phe	Ile 245	His	Met	Asn	Leu	Phe	Val 250	Ser	Phe	Met	Leu	Arg 255
Ala	Ile	Ser	Val 260	Phe	Ile	Lys	Asp	Trp 265	Ile	Leu	Tyr	Ala	Glu 270	Gln	Asp
Ser	Asn	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val

275					280					285					
Phe 290	Phe	His	Tyr	Cys	Val	Val 295	Ser	Asn	Tyr	Phe	Trp 300	Leu	Phe	Ile	Glu
Gly 305	Leu	Tyr	Leu	Phe	Thr 310	Leu	Leu	Val	Glu	Thr 315	Phe	Phe	Pro	Glu	Arg 320
Arg	Tyr	Phe	Tyr	Trp 325	Tyr	Thr	Ile	Ile	Gly 330	Trp	Gly	Thr	Pro	Thr 335	Val
Cys	Val	Thr	Val 340	Trp	Ala	Thr	Leu	Arg 345	Leu	Tyr	Phe	Asp	Asp 350	Thr	Gly
Cys	Trp	Asp 355	Met	Asn	Asp	Ser	Thr 360	Ala	Leu	Trp	Trp	Val 365	Ile	Lys	Gly
Pro 370	Val	Val	Gly	Ser	Ile	Met 375	Val	Asn	Phe	Val	Leu 380	Phe	Ile	Gly	Ile
Ile 385	Val	Ile	Leu	Val	Gln 390	Lys	Leu	Gln	Ser	Pro 395	Asp	Met	Gly	Gly	Asn 400
Glu	Ser	Ser	Ile	Tyr 405	Phe	Ser	Cys	Val	Gln 410	Lys	Cys	Tyr	Cys	Lys 415	Pro
Gln	Arg	Ala	Gln 420	Gln	His	Ser	Cys	Lys 425	Met	Ser	Glu	Leu	Ser	Thr 430	Ile
Thr	Leu	Arg 435	Leu	Ala	Arg	Ser	Thr 440	Leu	Leu	Leu	Ile	Pro 445	Leu	Phe	Gly
Ile 450	His	Tyr	Thr	Val	Phe	Ala 455	Phe	Ser	Pro	Glu	Asn 460	Val	Ser	Lys	Arg
Glu 465	Arg	Leu	Val	Phe	Glu 470	Leu	Gly	Leu	Gly	Ser 475	Phe	Gln	Gly	Phe	Val 480
Val	Ala	Val	Leu	Tyr 485	Cys	Phe	Leu	Asn	Gly 490	Glu	Val	Gln	Ala	Glu 495	Ile
Lys	Arg	Lys	Trp 500	Arg	Ser	Trp	Lys	Val 505	Asn	Arg	Tyr	Phe	Ala 510	Val	Asp
Phe	Lys	His 515	Arg	His	Pro	Ser	Leu 520	Ala	Ser	Ser	Gly	Val 525	Asn	Gly	Gly
Thr 530	Gln	Leu	Ser	Ile	Leu	Ser 535	Lys	Ser	Ser	Ser	Gln 540	Ile	Arg	Met	Ser
Gly 545	Leu	Pro	Ala	Asp	Asn 550	Leu	Ala	Thr							

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	1	5	10	15
Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp	Ser	Ser	Pro	20	25	30	
Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His	35	40	45	
Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	Phe	50	55	60	
Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Ser	Asp	Phe	65	70	75	
Gly	Asp	Ser	Asn	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	Arg	85	90	95	
Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	100	105	110	
Ala	Cys	Gly	Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	115	120	125	
Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	130	135	140	
Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	145	150	155	
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	165	170	175	
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	180	185	190	
Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys	Ala	195	200	205	

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	Ala	His	Cys	Gly	Ala	Cys	1	5	10	15
Pro	Trp	Gly	Arg	Gly	Arg	Leu	Arg	Lys	Gly	Arg	Ala	Ala	Cys	Lys	Ser	20	25	30	
Ala	Ala	Gln	Arg	His	Ile	Gly	Ala	Asp	Leu	Pro	Leu	Leu	Ser	Val	Gly	35	40	45	
Gly	Gln	Trp	Cys	Trp	Pro	Arg	Ser	Val	Met	Ala	Gly	Val	Val	His	Val	50	55	60	
Ser	Leu	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Met	Ala	Pro	Ala	Met	His	Ser	65	70	75	80
Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	85	90	95	
Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp	Ser	Ser	Pro	Gly	Cys	Pro	100	105	110	
Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His	Val	Gly	Glu	115	120	125	
Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	Phe	Asn	Pro	Asp	130	135	140	
Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Ser	Asp	Phe	Gly	Asp	Ser	145	150	155	160
Asn	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	Arg	Asn	Cys	Thr	165	170	175	
Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	Ala	Cys	Gly	180	185	190	
Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	Tyr	Tyr	Leu	195	200	205	
Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	210	215	220	

Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys
 225 230 235 240
 Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg
 245 250 255
 Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp
 260 265 270
 Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val
 275 280 285
 Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu
 290 295 300
 Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg
 305 310 315 320
 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val
 325 330 335
 Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly
 340 345 350
 Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile Lys Gly
 355 360 365
 Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile
 370 375 380
 Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn
 385 390 395 400
 Glu Ser Ser Ile Tyr Phe Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln
 405 410 415
 Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr
 420 425 430
 Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile
 435 440 445
 His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu
 450 455 460
 Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val
 465 470 475 480
 Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys
 485 490 495
 Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Ala Val Asp Phe

500	505	510
Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr		
515	520	525
Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly		
530	535	540
Leu Pro Ala Asp Asn Leu Ala Thr		
545	550	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
1				5					10					15	
Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp	Ser	Ser	Pro
			20					25					30		
Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His
		35					40					45			
Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	Phe
	50					55					60				
Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Ser	Asp	Phe
65					70					75					80
Gly	Asp	Ser	Asn	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	Arg
				85					90					95	
Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp
			100					105					110		
Ala	Cys	Gly	Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr
		115					120					125			
Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser
	130					135					140				
Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys

145					150					155					160
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe
				165					170					175	
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala
			180					185					190		
Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys	Ala
		195					200					205			
Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu
	210					215					220				
Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe
225					230					235					240
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr
				245					250					255	
Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Thr	Leu	Arg	Leu	Tyr	Phe	Asp
			260					265					270		
Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val
		275					280					285			
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe
	290					295					300				
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met
305					310					315				320	
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Thr	Asn	Leu	Ser	Pro	Arg	Val
				325					330					335	
Pro	Lys	Lys	Ala	Arg	Glu	Asp	Pro	Leu	Pro	Val	Pro	Ser	Asp	Gln	His
			340					345					350		
Ser	Leu	Pro	Phe	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro
		355					360					365			
Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val
						375					380				
Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln
385					390					395				400	
Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln
				405					410					415	
Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe
			420					425					430		

Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val
 435 440 445
 Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile
 450 455 460
 Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
 465 470 475

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys
 1 5 10 15
 Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser
 20 25 30
 Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu Leu Ser Val Gly
 35 40 45
 Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val
 50 55 60
 Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser
 65 70 75 80
 Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln
 85 90 95
 Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro
 100 105 110
 Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu
 115 120 125
 Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp
 130 135 140
 Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser
 145 150 155 160

Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr
165 170 175

Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly
180 185 190

Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu
195 200 205

Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr
210 215 220

Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys
225 230 235 240

Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg
245 250 255

Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp
260 265 270

Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val
275 280 285

Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu
290 295 300

Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg
305 310 315 320

Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val
325 330 335

Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly
340 345 350

Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile Lys Gly
355 360 365

Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile
370 375 380

Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn
385 390 395 400

Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg Val Pro Lys Lys
405 410 415

Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln His Ser Leu Pro
420 425 430

Phe Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly

FOUO 4-05600

435		440		445
Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg				
450		455		460
Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val				
465		470		475
Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile				
	485		490	495
Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Ala Val Asp				
	500		505	510
Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly				
	515		520	525
Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser				
	530		535	540
Gly Leu Pro Ala Asp Asn Leu Ala Thr				
545		550		

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGAGAGGCG GCGGCACTG GCCCGAGCCG CCTTGCAGGC TGAGAAGCGT CATGGCCAGC	60
ATCGCGCAGG TCTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCACCGC CATGCATTCC	120
GACTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGTGAATGAC	180
CTGATGGGCT TGAATGACTC CTCCCCAGGG TGCCCTGGGA TGTGGGACAA CATCACGTGT	240
TGGAAGCCCG CCCACGTGGG TGAGATGGTC CTGGTCAGTT GCCCTGAACT CTTCCGAATC	300
TTCAACCCAG ACCAAGTCTG GGAGACGGAA ACCATCGGAG AGTTCGGTTT TGCAGACAGT	360

AAATCCTTGG ATCTCTCAGA CATGAGGGTG GTGAGCCGGA ATTGCACGGA GGATGGATGG	420
TCAGAGCCAT TCCCTCATTA TTTCGATGCC TGTGGGTTTG AGGAGTACGA ATCTGAGACT	480
GGGGACCAGG ATTACTACTA CCTGTCAGTG AAGGCCCTGT ACACAGTTGG CTACAGCACG	540
TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTGTGTC GTTTCCGGAA GCTGCACTGC	600
ACCCGCAACT TCATCCACAT GAACCTCTTC GTGTCGTTTA TGCTGAGGGC CATCTCCGTC	660
TTCATCAAAG ACTGGATCCT CTATGCTGAG CAGGACAGCA ATCACTGCTT TGTCTCCACT	720
GTGGAATGCA AGGCTGTGAT GGTTTTCTTC CACTACTGTG TTGTATCCAA CTACTTCTGG	780
CTGTTTCATCG AGGGCCTGTA TCTCTTCACC CTGCTGGTGG AGACCTTCTT CCCCAGAGAGG	840
AGATATTTCT ACTGGTACAT CATCATTTGGC TGGGGGACAC CAACTGTGTG TGTGTCTGTG	900
TGGGCTATGC TGAGGCTCTA CTTCGATGAC ACAGGCTGCT GGGATATGAA TGACAACACG	960
GCTCTGTGGT GGGTGATCAA AGGCCCTGTA GTTGGCTCCA TAATGGTTAA TTTTGTGCTC	1020
TTTCATCGGCA TCATTGTCAT CCTTGTCAG AAACCTTCAGT CTCCAGACAT GGGAGGCAAC	1080
GAGTCCAGCA TCTACTTCAG CTGCGTGCAG AAATGCTACT GCAAGCCACA GCGGGCTCAG	1140
CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TACGGCTCGC CAGGTCCACC	1200
TTGCTGCTCA TCCCACTCTT TGGAATCCAC TACACTGTCT TTGCTTTCTC CCCGGAGAAC	1260
GTCAGCAAGA GGGAGAGACT GGTGTTTGAG CTGGGTCTGG GCTCCTTCCA GGGCTTTGTG	1320
GTGGCTGTTT TCTATTGCTT TCTGAATGGA GAGGTGCAGG CGGAGATCAA GAGGAAGTGG	1380
CGGAGCTGGA AGGTGAACCG CTACTTCACC ATGGACTTCA AGCACCGGCA CCCATCCCTG	1440
GCCAGCAGCG GGGTGAACGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAG	1500
ATCCGCATGT CTGGGCTTCC GGCCGACAAC CTGGCCACC	1539

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..1455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGAGAGGCG	GGCGGCACTG	GCCCGAGCCG	CCTTGCAGGC	TGAGAAGCGT	CATGGCCAGC	60
ATCGCGCAGG	TCTCCCTGGC	TGCTCTCCTC	CTGCTGCCTA	TGGCCACCGC	CATGCATTCC	120
GACTGCATCT	TCAAGAAGGA	GCAAGCCATG	TGCCTGGAGA	AGATCCAGAG	GGTGAATGAC	180
CTGATGGGCT	TGAATGACTC	CTCCCCAGGG	TGCCCTGGGA	TGTGGGACAA	CATCACGTGT	240
TGGAAGCCCG	CCCACGTGGG	TGAGATGGTC	CTGGTCAGTT	GCCCTGAACT	CTTCCGAATC	300
TTCAACCCAG	ACCAAGTCTG	GGAGACGGAA	ACCATCGGAG	AGTTCGGTTT	TGCAGACAGT	360
AAATCCTTGG	ATCTCTCAGA	CATGAGGGTG	GTGAGCCGGA	ATTGCACGGA	GGATGGATGG	420
TCAGAGCCAT	TCCCTCATTA	TTTCGATGCC	TGTGGGTTTG	AGGAGTACGA	ATCTGAGACT	480
GGGACACAGG	ATTACTACTA	CCTGTCAGTG	AAGGCCCTGT	ACACAGTTGG	CTACAGCACG	540
TCCCTCGTCA	CCCTCACCAC	TGCCATGGTC	ATCCTGTGTC	GTTTCCGGAA	GCTGCACTGC	600
ACCGCAACT	TCATCCACAT	GAACCTCTTC	GTGTCGTTTA	TGCTGAGGGC	CATCTCCGTC	660
TTGATCAAAG	ACTGGATCCT	CTATGCTGAG	CAGGACAGCA	ATCACTGCTT	TGTCTCCACT	720
GTGGAATGCA	AGGCTGTGAT	GGTTTTCTTC	CACTACTGTG	TTGTATCCAA	CTACTTCTGG	780
CTGTTCATCG	AGGGCCTGTA	TCTCTTCACC	CTGCTGGTGG	AGACCTTCTT	CCCCGAGAGG	840
AGATATTTCT	ACTGGTACAT	CATCATTGGC	TGGGGGACAC	CAACTGTGTG	TGTGTCTGTG	900
TGGGCTATGC	TGAGGCTCTA	CTTCGATGAC	ACAGGCTGCT	GGGATATGAA	TGACAACACG	960
GCTCTGTGGT	GGGTGATCAA	AGGCCCTGTA	GTTGGCTCCA	TAATGGTTAA	TTTTGTGCTC	1020
TTCATCGGCA	TCATTGTCAT	CCTTGTGCAG	AAACTTCAGT	CTCCAGACAT	GGGAGGCAAC	1080
GAGTCCAGCA	TCTACTTACG	GCTCGCCAGG	TCCACCTTGC	TGCTCATCCC	ACTCTTTGGA	1140
ATCCACTACA	CTGTCTTTGC	TTTCTCCCCG	GAGAACGTCA	GCAAGAGGGA	GAGACTGGTG	1200
TTTGAGCTGG	GTCTGGGCTC	CTTCCAGGGC	TTTGTGGTGG	CTGTTCTCTA	TTGCTTTCTG	1260
AATGGAGAGG	TGCAGGCGGA	GATCAAGAGG	AAGTGGCGGA	GCTGGAAGGT	GAACCGCTAC	1320
TTCACCATGG	ACTTCAAGCA	CCGGCACCCA	TCCCTGGCCA	GCAGCGGGGT	GAACGGGGGC	1380

ACCCAGCTCT CCATCCTGAG CAAGAGCAGC TCCCAGATCC GCATGTCTGG GCTTCCGGCC 1440
GACAACTGG CCACC 1455

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGCCAGAG TCCTGCAGCT CTCCCTGACT GCTCTCCTGC TGCCTGTGGC TATTGCTATG	60
CAGTCTGACT GCATCTTCAA GAAGGAGCAA GCCATGTGCC TGGAGAGGAT CCAGAGGGCC	120
AAGGACCTGA TGGGACTAAA CGAGTCTTCC CCAGGTTGCC CTGGCATGTG GGACAATATC	180
ACATGTTGGA AGCCAGCTCA AGTAGGTGAG ATGGTCCTTG TAAGCTGCCC TGAGGTCTTC	240
CGCATCTTCA ACCCGGACCA AGTCTGGATG ACAGAAACCA TAGGAGATTC TGGTTTTGCC	300
GATAGTAATT CCTTGGAGAT CACAGACATG GGGGTCGTGG GCCGGAAGTG CACAGAGGAC	360
GGCTGGTCCG AGCCCTTCCC CCACTACTTC GATGCTTG TGTTTGATGA TTATGAGCCT	420
GAGTCTGGAG ATCAGGATTA TTACTACCTG TCGGTGAAGG CTCTCTACAC AGTCGGCTAC	480
AGCACTTCCC TCGCCACCCT CACTACTGCC ATGGTCATCT TGTGCCGCTT CCGGAAGCTG	540
CATTGCACTC GCAACTTCAT CCACATGAAC CTGTTTGTAT CCTTCATGCT GAGGGCTATC	600
TCCGTCTTCA TCAAGGACTG GATCTTGATC GCCGAGCAGG ACAGCAGTCA CTGCTTCGTT	660
TCCACCGTGG AGTGCAAAGC TGTCATGGTT TTCTTCCACT ACTGCGTGGT GTCCAAGTAC	720
TTCTGGCTGT TCATTGAAGG CCTGTACCTC TTTACACTGC TGGTGGAGAC CTTCTTCCCT	780
GAGAGGAGAT ATTTCTACTG GTACACCATC ATCGGCTGGG GGACACCTAC TGTGTGTGTA	840
ACAGTGTGGG CTGTGCTGAG GCTCTATTTT GATGATGCAG GATGCTGGGA TATGAATGAC	900

AGCACAGCTC TGTGGTGGGT GATCAAAGGC CCCGTGGTTG GCTCTATAAT GGTAACTTT	960
GTGCTTTTCA TCGGCATCAT CATCATCCTT GTACAGAAGC TGCAGTCCCC AGACATGGGA	1020
GGCAACGAGT CCAGCATCTA CTTACGGCTG GCCCGCTCCA CCCTACTGCT CATCCCCTC	1080
TTCGGAATCC ACTACACAGT ATTCGCCTTC TCTCCAGAGA ACGTCAGCAA GAGGGAAAGA	1140
CTTGTGTTTG AGCTTGGGCT GGGCTCCTTC CAGGGCTTTG TGGTGGCTGT ACTCTACTGC	1200
TTCCTGAATG GGGAGGTACA GGCAGAGATT AAGAGGAAAT GGAGGAGCTG GAAGGTGAAC	1260
CGTTACTTCA CTATGGACTT CAAGCACCGG CACCCGTCCC TGGCCAGCAG TGGAGTAAAT	1320
GGGGGAACCC AGCTGTCCAT CCTGAGCAAG AGCAGCTCCC AGCTCCGCAT GTCCAGCCTC	1380
CCGGCCGACA ACTTGGCCAC C	1401

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGCCAGAG TCCTGCAGCT CTCCCTGACT GCTCTCCTGC TGCCTGTGGC TATTGCTATG	60
CACTCTGACT GCATCTTCAA GAAGGAGCAA GCCATGTGCC TGGAGAGGAT CCAGAGGGCC	120
AACGACCTGA TGGGACTAAA CGAGTCTTCC CCAGGTTGCC CTGGCATGTG GGACAATATC	180
ACATGTTGGA AGCCAGCTCA AGTAGGTGAG ATGGTCCTTG TAAGCTGCCC TGAGGTCTTC	240
CGGATCTTCA ACCCGGACCA AGTCTGGATG ACAGAAACCA TAGGAGATTG TGGTTTTGCC	300
GATAGTAATT CCTTGGAGAT CACAGACATG GGGGTCGTGG GCCGGAACCTG CACAGAGGAC	360
GGCTGGTCGG AGCCCTTCCC CCACTACTTC GATGCTTGTTG GGTGTTGATGA TTATGAGCCT	420
GAGTCTGGAG ATCAGGATTA TTACTACCTG TCGGTGAAGG CTCTCTACAC AGTCGGCTAC	480

AGCACTTCCC TCGCCACCCT CACTACTGCC ATGGTCATCT TGTGCCGCTT CCGGAAGCTG	540
CATTGCACTC GCAACTTCAT CCACATGAAC CTGTTTGTAT CCTTCATGCT GAGGGCTATC	600
TCCGTCTTCA TCAAGGACTG GATCTTGTAC GCCGAGCAGG ACAGCAGTCA CTGCTTCGTT	660
TCCACCGTGG AGTGCAAAGC TGTCATGGTT TTCTTCCACT ACTGCGTGGT GTCCAACTAC	720
TTCTGGCTGT TCATTGAAGG CCTGTACCTC TTTACACTGC TGGTGGAGAC CTTCTTCCCT	780
GAGAGGAGAT ATTTCTACTG GTACACCATC ATCGGCTGGG GGACACCTAC TGTGTGTGTA	840
ACAGTGTGGG CTGTGCTGAG GCTCTATTTT GATGATGCAG GATGCTGGGA TATGAATGAC	900
AGCACAGCTC TGTGGTGGGT GATCAAAGGC CCCGTGGTTG GCTCTATAAT GGTTAACTTT	960
GTGCTTTTCA TCGGCATCAT CATCATCCTT GTACAGAAGC TGCAGTCCCC AGACATGGGA	1020
GGCAACGAGT CCAGCATCTA CTTCAGCTGC GTGCAGAAAT GCTACTGCAA GCCACAGCGG	1080
GCTCAGCAGC ACTCTTGCAA GATGTCAGAA CTATCCACCA TTACTCTACG GCTGGCCCCG	1140
TCCACCCTAC TGCTCATCCC ACTCTTCGGA ATCCACTACA CAGTATTCGC CTTCTCTCCA	1200
GACAACGTCA GCAAGAGGGA AAGACTTGTG TTTGAGCTTG GGCTGGGCTC CTTCCAGGGC	1260
TTTGTGGTGG CTGTACTCTA CTGCTTCCTG AATGGGGAGG TACAGGCAGA GATTAAGAGG	1320
AAATGGAGGA GCTGGAAGGT GAACCGTTAC TTCACTATGG ACTTCAAGCA CCGGCACCCG	1380
TCCCTGGCCA GCAGTGGAGT AAATGGGGGA ACCCAGCTGT CCATCCTGAG CAAGAGCAGC	1440
TCCCAGCTCC GCATGTCCAG CCTCCCGGCC GACAACTTGG CCACC	1485

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATGGCTGGTG	TCGTGCACGT	TTCCCTGGCT	GCTCACTGCG	GGGCCTGTCC	GTGGGGCCGG	60
GGCAGACTCC	GCAAAGGACG	CGCAGCCTGC	AAGTCCGCGG	CCCAGAGACA	CATTGGGGCT	120
GACCTGCCCG	TGCTGTCAGT	GGGAGGCCAG	TGGTGCTGGC	CAAGAAGTGT	CATGGCTGGT	180
GTCGTGCACG	TTTCCCTGGC	TGCTCTCCTC	CTGCTGCCTA	TGGCCCCTGC	CATGCATTCT	240
GACTGCATCT	TCAAGAAGGA	GCAAGCCATG	TGCCTGGAGA	AGATCCAGAG	GGCCAATGAG	300
CTGATGGGCT	TCAATGATTC	CTCTCCAGGC	TGTCCTGGGA	TGTGGGACAA	CATCACGTGT	360
TGGAAGCCCCG	CCCATGTGGG	TGAGATGGTC	CTGGTCAGCT	GCCCTGAGCT	CTTCCGAATC	420
TTCAACCCAG	ACCAAGTCTG	GGAGACCGAA	ACCATTGGAG	AGTCTGATTT	TGGTGACAGT	480
AACTCCTTAG	ATCTCTCAGA	CATGGGAGTG	GTGAGCCGGA	ACTGCACGGA	GGATGGCTGG	540
TGGGAACCCT	TCCCTCATTA	CTTTGATGCC	TGTGGGTTTG	ATGAATATGA	ATCTGAGACT	600
GGGGACCAGG	ATTATTACTA	CCTGTCAGTG	AAGGCCCTCT	ACACGGTTGG	CTACAGCACA	660
TGCTCGTCA	CCCTCACCAC	TGCCATGGTC	ATCCTTTGTC	GCTTCCGGAA	GCTGCACTGC	720
ACACGCAACT	TCATCCACAT	GAACCTGTTT	GTGTCGTTCA	TGCTGAGGGC	GATCTCCGTC	780
TTTATCAAAG	ACTGGATTCT	GTATGCGGAG	CAGGACAGCA	ACCACTGCTT	CATCTCCACT	840
GTGGAATGTA	AGGCCGTCAT	GGTTTTCTTC	CACTACTGTG	TTGTGTCCAA	CTACTTCTGG	900
CTGTTTCATCG	AGGGCCTGTA	CCTCTTCACT	CTGCTGGTGG	AGACCTTCTT	CCCTGAAAGG	960
AGATACTTCT	ACTGGTACAC	CATCATTTGGC	TGGGGGTCCC	CAACTGTGTG	TGTGACAGTG	1020
TGGGCTACGC	TGAGACTCTA	CTTTGATGAC	ACAGGCTGCT	GGGATATGAA	TGACAGCACA	1080
GCTCTGTGGT	GGGTGATCAA	AGGCCCTGTG	GTTGGCTCTA	TCATGGTTAA	CTTTGTGCTT	1140
TTTATTGGCA	TTATCGTCAT	CCTTGTGCAG	AAACTTCAGT	CTCCAGACAT	GGGAGGCAAT	1200
GAGTCCAGCA	TCTACTTGCG	ACTGGCCCCG	TCCACCCTGC	TGCTCATCCC	ACTATTGCGA	1260
ATCCACTACA	CAGTATTTGC	CTTCTCCCCA	GAGAATGTCA	GCAAAAGGGA	AAGACTCGTG	1320
TTTGAGCTGG	GGCTGGGCTC	CTTCCAGGGC	TTTGTGGTGG	CTGTTCTCTA	CTGTTTTCTG	1380
AATGGTGAGG	TACAAGCGGA	GATCAAGCGA	AAATGGCGAA	GCTGGAAGGT	GAACCGTTAC	1440
TTGCTGTGG	ACTTCAAGCA	CCGACACCCG	TCTCTGGCCA	GCAGTGGGGT	GAATGGGGGC	1500
ACCCAGCTCT	CCATCCTGAG	CAAGAGCAGC	TCCCAAATCC	GCATGTCTGG	CCTCCCTGCT	1560

1575

GACAATCTGG CCACC

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1659 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGCTGGTG TCGTGCACGT TTCCCTGGCT GCTCACTGCG GGCCTGTCC GTGGGGCCGG	60
GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTGGGGCT	120
GAGCTGCCGC TGCTGTCACT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT	180
GTCGTGCACG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCCTGC CATGCATTCT	240
GAGTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG	300
CTGATGGGCT TCAATGATTCTCTCCAGGC TGTCTGGGA TGTGGGACAA CATCACGTGT	360
TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC	420
TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT	480
AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGGA ACTGCACGGA GGATGGCTGG	540
TCGGAACCCT TCCCTCATTA CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT	600
GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA	660
TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC	720
ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC	780
TTCATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT	840
GTGGAATGTA AGGCCGTCAT GGTCTTCTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG	900
CTGTTTCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG	960

AGATACTTCT ACTGGTACAC CATCATTTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG	1020
TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA	1080
GCTCTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT	1140
TTTATTGGCA TTATCGTCAT CCTTGTGCAG AACTTTCAGT CTCCAGACAT GGGAGGCAAT	1200
GAGTCCAGCA TCTACTTCAG CTGCGTGCAG AAATGCTACT GCAAGCCACA GCGGGCTCAG	1260
CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TGCGACTGGC CCGGTCCACC	1320
CTGCTGCTCA TCCCACTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC CCCAGAGAAT	1380
GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA GGGCTTTGTG	1440
GTGGCTGTTC TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA GCGAAAATGG	1500
CGAAGCTGGA AGGTGAACCG TTA CTTCGCT GTGGACTTCA AGCACCGACA CCCGTCTCTG	1560
GCGAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAA	1620
ATCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACC	1659

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGGCTGGTG TCGTGACAGT TTCCCTGGCT GCTCACTGCG GGGCCTGTCC GTGGGGCCGG	60
GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTGGGGCT	120
GACCTGCCGC TGCTGTCAGT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT	180
GTCGTGCACG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCTGC CATGCATTCT	240
GA CTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG	300

CTGATGGGCT TCAATGATTC CTCTCCAGGC TGTCTGGGA TGTGGGACAA CATCACGTGT	360
TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC	420
TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT	480
AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGA ACTGCACGGA GGATGGCTGG	540
TCGGAACCCT TCCCTCATTA CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT	600
GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA	660
TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC	720
ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC	780
TTTATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT	840
GTGGAATGTA AGGCCGTCAT GGTTTTCTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG	900
CTGATCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG	960
AGATACTTCT ACTGGTACAC CATCATTTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG	1020
TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA	1080
GCTGTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT	1140
TTTATTGGCA TTATCGTCAT CCTTGTGCAG AACTTTCAGT CTCCAGACAT GGGAGGCAAT	1200
GAGTCCAGCA TCTACTTCTG CGTGCAGAAA TGCTACTGCA AGCCACAGCG GGCTCAGCAG	1260
CACTCTTGCA AGATGTCAGA ACTGTCCACC ATTACTCTGC GACTGGCCCG GTCCACCCTG	1320
CTGCTCATCC CACTATTCGG AATCCACTAC ACAGTATTTG CCTTCTCCCC AGAGAATGTC	1380
AGCAAAAGGG AAAGACTCGT GTTTGAGCTG GGGCTGGGCT CCTTCCAGGG CTTTGTGGTG	1440
GCTGTTCTCT ACTGTTTTCT GAATGGTGAG GTACAAGCGG AGATCAAGCG AAAATGGCGA	1500
AGCTGGAAGG TGAACCGTTA CTTGCTGTG GACTTCAAGC ACCGACACCC GTCTCTGGCC	1560
AGCAGTGGGG TGAATGGGGG CACCCAGCTC TCCATCCTGA GCAAGAGCAG CTCCCAAATC	1620
CGCATGTCTG GCCTCCCTGC TGACAATCTG GCCACC	1656

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGGCTGGTG TCGTGCACGT TTCCCTGGCT GCTCACTGCG GGGCCTGTCC GTGGGGCCGG	60
GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTGGGGCT	120
GACCTGCCGC TGCTGTCACT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT	180
GTGGTGCACG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCTGC CATGCATTCT	240
GAGTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG	300
CTGATGGGCT TCAATGATTC CTCTCCAGGC TGTCCTGGGA TGTGGGACAA CATCACGTGT	360
TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC	420
TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT	480
AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGGA ACTGCACGGA GGATGGCTGG	540
TGGGAACCCT TCCCTCATTA CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT	600
GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA	660
TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC	720
ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC	780
TTCATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT	840
GTGGAATGTA AGGCCGTCAT GGTTTTCTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG	900
CTGTTTCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG	960
AGATACTTCT ACTGGTACAC CATCATTTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG	1020
TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA	1080
GCTCTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT	1140
TTTATTGGCA TTATCGTCAT CCTTGTGCAG AACTTCAGT CTCCAGACAT GGGAGGCAAT	1200

GAGTCCAGCA TCTACTTAAC AAATTTAAGC CCGCGAGTCC CCAAGAAAGC CCGAGAGGAC	1260
CCCCTGCCTG TGCCCTCAGA CCAGCATTCA CTCCCTTTCC TGCGACTGGC CCGGTCCACC	1320
CTGCTGCTCA TCCCCTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC CCCAGAGAAT	1380
GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA GGGCTTTGTG	1440
GTGGCTGTTT TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA GCGAAAATGG	1500
CGAAGCTGGA AGGTGAACCG TTACTTCGCT GTGGACTTCA AGCACCGACA CCCGTCTCTG	1560
GCCAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAA	1620
ATCCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACC	1659

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 498..2036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGGCCTGCAC CCCACCCCCC AGCCTGCGAA GACGGGGGGA GGCGGTGGTC GGTCGCCTCC	60
CTCCTGCCCC CGGCCTGGCT TCGCGGTGGA GGCGGTGCCT CTCCGGCAAG GCAGACCAGG	120
CTGGGCGGAC GCGCGGCGCG GGGCGGGCTA GGGAAGGCCG GGGGCCTCGC GCTCGGGCCC	180
CGGGCGGCGA CTGACAGCGG CGGCGGCGGC GGCAGCGGCT CCAAGGCGAG CGTGGTCCCC	240
GCGTGCGCAC AAGCTCGCCG CCGCGCAGGG ACCCACGGAC ACCGGCGCCG GCGGGACACA	300
CAGACGCGGA GATCGGGCTC TACGCGCGCT ACTCAGCGCA CGAGCTCCCC ATCCCTGGGC	360
GGAGCGGGGC GCGGACTCGC CGCTGCGCGC CCTCCCCGCG GAGTCTGCCC CGGGCAGACC	420
CGCAGCCCCG GGGCCCCGCC CGAGGCCCTT GGGTGAGCAG CCTGTAGACA CCTGGGGTTG	480
AGCAGTGGCG GCTGTGAATG AGAGGCGGGC GGCAGTGGCC CGAGCCGCCT TGCAGGCTGA	540

GAAGCGTCAT	GGCCAGCATC	GCGCAGGTCT	CCCTGGCTGC	TCTCCTCCTG	CTGCCTATGG	600
CCACCGCCAT	GCATTCCGAC	TGCATCTTCA	AGAAGGAGCA	AGCCATGTGC	CTGGAGAAGA	660
TCCAGAGGGT	GAATGACCTG	ATGGGCTTGA	ATGACTCCTC	CCCAGGGTGC	CCTGGGATGT	720
GGGACAACAT	CACGTGTTGG	AAGCCCGCCC	ACGTGGGTGA	GATGGTCCTG	GTCAGTTGCC	780
CTGAACTCTT	CCGAATCTTC	AACCCAGACC	AAGTCTGGGA	GACGGAAACC	ATCGGAGAGT	840
TCGGTTTTGC	AGACAGTAAA	TCCTTGGATC	TCTCAGACAT	GAGGGTGGTG	AGCCGGAATT	900
GCACGGAGGA	TGGATGGTCA	GAGCCATTCC	CTCATTTATTT	CGATGCCTGT	GGGTTTGAGG	960
AGTACGAATC	TGAGACTGGG	GACCAGGATT	ACTACTACCT	GTCAGTGAAG	GCCCTGTACA	1020
CAGTTGGCTA	CAGCACGTCC	CTCGTCACCC	TCACCACTGC	CATGGTCATC	CTGTGTCGTT	1080
TCCGGAAGCT	GCACTGCACC	CGCAACTTCA	TCCACATGAA	CCTCTTCGTG	TCGTTTATGC	1140
TGAGGGCCAT	CTCCGTCTTC	ATCAAAGACT	GGATCCTCTA	TGCTGAGCAG	GACAGCAATC	1200
ACTGCTTTGT	CTCCACTGTG	GAATGCAAGG	CTGTGATGGT	TTTCTTCCAC	TACTGTGTTG	1260
TATCCAATA	CTTCTGGCTG	TTCATCGAGG	GCCTGTATCT	CTTCACCCTG	CTGGTGGAGA	1320
CCTTCTTCCC	CGAGAGGAGA	TATTTCTACT	GGTACATCAT	CATTGGCTGG	GGGACACCAA	1380
CTGTGTGTGT	GTCTGTGTGG	GCTATGCTGA	GGCTCTACTT	CGATGACACA	GGCTGCTGGG	1440
ATATGAATGA	CAACACGGCT	CTGTGGTGGG	TGATCAAAGG	CCCTGTAGTT	GGCTCCATAA	1500
TGGTTAATTT	TGTGCTCTTC	ATCGGCATCA	TTGTCATCCT	TGTGCAGAAA	CTTCAGTCTC	1560
CAGACATGGG	AGGCAACGAG	TCCAGCATCT	ACTTCAGCTG	CGTGCAGAAA	TGCTACTGCA	1620
AGCCACAGCG	GGCTCAGCAG	CACTCTTGCA	AGATGTCAGA	ACTGTCCACC	ATTACTCTAC	1680
GGCTCGCCAG	GTCCACCTTG	CTGCTCATCC	CACTCTTTGG	AATCCACTAC	ACTGTCTTTG	1740
CTTTCTCCCC	GGAGAACGTC	AGCAAGAGGG	AGAGACTGGT	GTTTGAGCTG	GGTCTGGGCT	1800
CCTTCCAGGG	CTTTGTGGTG	GCTGTTCTCT	ATTGCTTTCT	GAATGGAGAG	GTGCAGGCGG	1860
AGATCAAGAG	GAAGTGGCGG	AGCTGGAAGG	TGAACCGCTA	CTTCACCATG	GACTTCAAGC	1920
ACCGGCACCC	ATCCCTGGCC	AGCAGCGGGG	TGAACGGGGG	CACCCAGCTC	TCCATCCTGA	1980
GCAAGAGCAG	CTCCCAGATC	CGCATGTCTG	GGCTTCCGGC	CGACAACCTG	GCCACCTGAG	2040
CCCACCCTGC	CCCCTCCTCT	CCTCTGTACG	CAGGCTGGGG	CTGTGGTGGG	GCGCCGGCCC	2100

ACGCATGTTG TGCCTCTTCT CGCCTTCGGG CAGGCCCCGG GCTGGGCGCC TGGCCCCCGA	2160
GGTTGGAGAA GGATGCGGGA CAGGCAGCTG TTTAGCCTTC CTGTTTTGGC GCTGGCCCAA	2220
CCACCGTGGG TCCCTGGGCC TGCACCCAGA CATGTAATAC TCCTTAATTG GGAAGTCATC	2280
CATTCTTTCC CTTTCCCAAG TCCTTGCTTA TTAAGAGGTT CAAGTCACCT ACCCAATTCA	2340
GAAGCTTAAG TAACCACTAA CCACCGTGAC TGCCTGGGAG GCCTCCCATG GGCTGAGCTA	2400
CTGACTTGGC TTTGGGGGCC TTGGGCTGGG GCCCTCCTTA AAGCCCCCCC TGAAATTGTC	2460
GGACCTCAAA GTGTGACTCC TTTGAGTCTA CTCGCCACCC CCGTGGCCCT TTGCAGCCCT	2520
GGTCCAGTCA CCGAGGTTAC TGGAAGTCCA GCTTGGATGG CCAGACAGCT TTTTGGCACA	2580
GGCAGACCCA TGCTCACCCA ACATTTTAGT GTCCAGGTGC CCAGGTGCCC AGGTGCCCAG	2640
CTCCTGGGCA TCAGACAGTG GGAAAGCTCC AGGGATCTAC CATTTCAGAGA CTTTCAGTTTG	2700
GATGTAGGGC TAAGGCCAGA GAAAAGTTCT GGAGCTTTTC ATTTGGCCCA AGAAAAAACT	2760
GCCAGATCC AGAAAAGTGG ATCTGAGTGG AATTTAGATG CAAAGAGCTT GGAG	2814

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 498..1952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TGGCCTGCAC CCCACCCCCC AGCCTGCGAA GACGGGGGGA GGCGGTGGTC GGTCGCCTCC	60
CTCCTGCCCC CGGCCTGGCT TCGCGGTGGA GGCGGTGCCT CTCCGGCAAG GCAGACCAGG	120
CTGGGCGGAC GCGCGGCGCG GGGCGGGCTA GGGAAGGCCG GGGGCCTCGC GCTCGGGCCC	180
CGGGCGGCGA CTGACAGCGG CGGCGGCGGC GGCAGCGGCT CCAAGGCGAG CGTGGTCCCC	240
GCGTGCGCAC AAGCTCGCCG CCGCGCAGGG ACCCAGGAC ACCGGCGCCG GGCGGACACA	300

CAGACGCGGA	GATCGGGCTC	TACGCGCGCT	ACTCAGCGCA	CGAGCTCCCC	ATCCCTGGGC	360
GGAGCGGGGC	GCGGACTCGC	CGCTGCGCGC	CCTCCCCGCG	GAGTCTGCCC	CGGGCAGACC	420
CGCAGCCCGC	GGCCCCGCCG	CGAGGCCCCCT	GGGTGAGCAG	CCTGTAGACA	CCTGGGGTTG	480
AGCAGTGGCG	GCTGTGAATG	AGAGGCGGGC	GGCACTGGCC	CGAGCCGCCT	TGCAGGCTGA	540
GAAGCGTCAT	GGCCAGCATC	GCGCAGGTCT	CCCTGGCTGC	TCTCCTCCTG	CTGCCTATGG	600
CCACCGCCAT	GCATTCCGAC	TGCATCTTCA	AGAAGGAGCA	AGCCATGTGC	CTGGAGAAGA	660
TCCAGAGGGT	GAATGACCTG	ATGGGCTTGA	ATGACTCCTC	CCCAGGGTGC	CCTGGGATGT	720
GGGACAACAT	CACGTGTTGG	AAGCCCGCCC	ACGTGGGTGA	GATGGTCCTG	GTCAGTTGCC	780
CTGAACTCTT	CCGAATCTTC	AACCCAGACC	AAGTCTGGGA	GACGGAAACC	ATCGGAGAGT	840
TCGGTTTTC	AGACAGTAAA	TCCTTGGATC	TCTCAGACAT	GAGGGTGGTG	AGCCGGAATT	900
GCACGGAGGA	TGGATGGTCA	GAGCCATTCC	CTCATTATTT	CGATGCCTGT	GGGTTTGAGG	960
AGTACGAATC	TGAGACTGGG	GACCAGGATT	ACTACTACCT	GTCAGTGAAG	GCCCTGTACA	1020
CAGTTGGCTA	CAGCACGTCC	CTCGTCACCC	TCACCACTGC	CATGGTCATC	CTGTGTCGTT	1080
TCCGGAAGCT	GCACTGCACC	CGCAACTTCA	TCCACATGAA	CCTCTTCGTG	TCGTTTATGC	1140
TGAGGGCCAT	CTCCGTCTTC	ATCAAAGACT	GGATCCTCTA	TGCTGAGCAG	GACAGCAATC	1200
ACTGCTTTGT	CTCCACTGTG	GAATGCAAGG	CTGTGATGGT	TTTCTTCCAC	TACTGTGTTG	1260
TATCCAAC TA	CTTCTGGCTG	TTCATCGAGG	GCCTGTATCT	CTTCACCCTG	CTGGTGGAGA	1320
CCTTCTTCCC	CGAGAGGAGA	TATTTCTACT	GGTACATCAT	CATTGGCTGG	GGGACACCAA	1380
CTGTGTGTGT	GTCTGTGTGG	GCTATGCTGA	GGCTCTACTT	CGATGACACA	GGCTGCTGGG	1440
ATATGAATGA	CAACACGGCT	CTGTGGTGGG	TGATCAAAGG	CCCTGTAGTT	GGCTCCATAA	1500
TGGTTAATTT	TGTGCTCTTC	ATCGGCATCA	TTGTCATCCT	TGTGCAGAAA	CTTCAGTCTC	1560
CAGACATGGG	AGGCAACGAG	TCCAGCATCT	ACTTACGGCT	CGCCAGGTCC	ACCTTGCTGC	1620
TCATCCCACT	CTTTGGAATC	CACTACACTG	TCTTTGCTTT	CTCCCCGGAG	AACGTCAGCA	1680
AGAGGGAGAG	ACTGGTGTTT	GAGCTGGGTC	TGGGCTCCTT	CCAGGGCTTT	GTGGTGGCTG	1740
TTCTCTATTG	CTTTCTGAAT	GGAGAGGTGC	AGGCGGAGAT	CAAGAGGAAG	TGGCGGAGCT	1800
GGAAGGTGAA	CCGCTACTTC	ACCATGGACT	TCAAGCACCG	GCACCCATCC	CTGGCCAGCA	1860

GCGGGGTGAA CCGGGGCACC CAGCTCTCCA TCCTGAGCAA GAGCAGCTCC CAGATCCGCA	1920
TGTCTGGGCT TCCGGCCGAC AACCTGGCCA CCTGAGCCCA CCCTGCCCCC TCCTCTCCTC	1980
TGTACGCAGG CTGGGGCTGT GGTGGGGCGC CGGCCCACGC ATGTTGTGCC TCTTCTCGCC	2040
TTCGGGCAGG CCCC GGCTG GCGCCTGGC CCCC GAGGTT GGAGAAGGAT GCGGGACAGG	2100
CAGCTGTTTA GCCTTCCTGT TTTGGCGCTG GCCCAACCAC CGTGGGTCCC TGGGCCTGCA	2160
CCCAGACATG TAATACTCCT TAATTGGGAA GTCATCCATT CTTTCCCTTT CCCAAGTCCT	2220
TGCTTATTAA GAGGTTCAAG TCACCTACCC AATTCAGAAG CTTAAGTAAC CACTAACCAC	2280
CGTGACTGCG TGGGAGGCCT CCCATGGGCT GAGCTACTGA CTTGGCTTTG GGGGCCTTGG	2340
GCTGGGGCCC TCCTTAAAGC CCCCCCTGAA ATTGTCGGAC CTCAAAGTGT GACTCCTTTG	2400
AGTCTACTCG CCACCCCCGT GGCCCTTTGC AGCCCTGGTC CAGTCACCGA GGTTACTGGA	2460
AGTCCAGCTT GGATGGCCAG ACAGCTTTTTT GGCACAGGCA GACCCATGCT CACCCAACAT	2520
TTTAGTGTCC AGGTGCCCAG GTGCCCAGGT GCCCAGCTCC TGGGCATCAG ACAGTGGGAA	2580
AGTCCAGGG ATCTACCATT CAGAGACTTC AGTTTGATG TAGGGCTAAG GCCAGAGAAA	2640
AGTCTGGAG CTTTTCATTT GGCCCAAGAA AAAACTGCCA AGATCCAGAA AAGTGGATCT	2700
GAGTGGAATT TAGATGCAAA GAGCTTGGAG	2730

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 77..1477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA	60
GTGGCTGGGA AGCACCATGG CCAGAGTCCT GCAGCTCTCC CTGACTGCTC TCCTGCTGCC	120

TGTGGCTATT GCTATGCACT CTGACTGCAT CTTCAAGAAG GAGCAAGCCA TGTGCCTGGA	180
GAGGATCCAG AGGGCCAACG ACCTGATGGG ACTAAACGAG TCTTCCCCAG GTTGCCCTGG	240
CATGTGGGAC AATATCACAT GTTGGAAGCC AGCTCAAGTA GGTGAGATGG TCCTTGTAAG	300
CTGCCCTGAG GTCTTCCGGA TCTTCAACCC GGACCAAGTC TGGATGACAG AAACCATAGG	360
AGATTCTGGT TTTGCCGATA GTAATTCCTT GGAGATCACA GACATGGGGG TCGTGGGCCG	420
GAAGTGCACA GAGGACGGCT GGTCGGAGCC CTTCCCCAC TACTTCGATG CTTGTGGGTT	480
TGATGATTAT GAGCCTGAGT CTGGAGATCA GGATTATTAC TACCTGTCGG TGAAGGCTCT	540
CTACACAGTC GGCTACAGCA CTTCCCTCGC CACCCTCACT ACTGCCATGG TCATCTTGTG	600
CCGCTTCCGG AAGCTGCATT GCACTCGCAA CTTTCATCCAC ATGAACCTGT TTGTATCCTT	660
CATGCTGAGG GCTATCTCCG TCTTCATCAA GGACTGGATC TTGTACGCCG AGCAGGACAG	720
CAGTCACTGC TTCGTTTCCA CCGTGGAGTG CAAAGCTGTC ATGGTTTTCT TCCACTACTG	780
CGTGGTGTCC AACTACTTCT GGCTGTTTAT TGAAGGCCTG TACCTCTTTA CACTGCTGGT	840
GGAGACCTTC TTCCCTGAGA GGAGATATTT CTACTGGTAC ACCATCATCG GCTGGGGGAC	900
ACCTACTGTG TGTGTAACAG TGTGGGCTGT GCTGAGGCTC TATTTTGATG ATGCAGGATG	960
CTGGGATATG AATGACAGCA CAGCTCTGTG GTGGGTGATC AAAGGCCCG TGGTTGGCTC	1020
TATAATGGTT AACCTTGTGC TTTTCATCGG CATCATCATC ATCCTTGTAC AGAAGCTGCA	1080
GTCCCCAGAC ATGGGAGGCA ACGAGTCCAG CATCTACTTA CGGCTGGCCC GCTCCACCCT	1140
ACTGCTCATC CCACTCTTCG GAATCCACTA CACAGTATTC GCCTTCTCTC CAGAGAACGT	1200
CAGCAAGAGG GAAAGACTTG TGTTTGAGCT TGGGCTGGGC TCCTTCCAGG GCTTTGTGGT	1260
GGCTGTACTC TACTGCTTCC TGAATGGGGA GGTACAGGCA GAGATTAAGA GGAAATGGAG	1320
GAGCTGGAAG GTGAACCGTT ACTTCACTAT GGACTTCAAG CACCGGCACC CGTCCCTGGC	1380
CAGCAGTGA GTAAATGGGG GAACCCAGCT GTCCATCCTG AGCAAGAGCA GCTCCCAGCT	1440
CCGCATGTCC AGCCTCCCGG CCGACAACTT GGCCACCTGA GGCCTGTCTC CCTCCTCCTT	1500
CTGCACAGGC TGGGGCTGCG GGCCAGTGCC TGAGCATGTT TGTGCCTCTC CCCTCTCCTT	1560
GGGCAGGCCC TGGGTAGGAA GCTGGGCTCC TCCCCAAAGG GGAAGAGAGA GATAGGGTAT	1620
AGGCTGATAT TGCTCCTCCT GTTGGGTCC CACCTACTGT GATTCATTGA GCCTGATTTG	1680

ACATGTAAAT ACACCTCAAA TTTGGAAAGT TGCCCCATCT CTGCCCCCAA CCCATGCCCC	1740
TGCTCACCTC TGCCAGGCCC CAGCTCAACC TACTGTGTCA AGGCCAGCCT CAGTGATAGT	1800
CTGATCCCAG GTACAAGGCC TTGTGAGCTG AGGCTGAAAG GCCTGTTTTG GAGAGGCTGG	1860
GGTAGTGCC	1869

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 77..1561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA	60
GTGGCTGGGA AGCACCATGG CCAGAGTCCT GCAGCTCTCC CTGACTGCTC TCCTGCTGCC	120
TGTGGCTATT GCTATGCACT CTGACTGCAT CTTCAAGAAG GAGCAAGCCA TGTGCCTGGA	180
GAGGATCCAG AGGGCCAACG ACCTGATGGG ACTAAACGAG TCTTCCCCAG GTTGCCCTGG	240
CATGTGGGAC AATATCACAT GTTGGAAGCC AGCTCAAGTA GGTGAGATGG TCCTTGTAAG	300
CTGCCCTGAG GTCTTCCGGA TCTTCAACCC GGACCAAGTC TGGATGACAG AAACCATAGG	360
AGATTCTGGT TTTGCCGATA GTAATTCCTT GGAGATCACA GACATGGGGG TCGTGGGCCG	420
GAACTGCACA GAGGACGGCT GGTCGGAGCC CTTCCCCCAC TACTTCGATG CTTGTGGGTT	480
TGATGATTAT GAGCCTGAGT CTGGAGATCA GGATTATTAC TACCTGTCGG TGAAGGCTCT	540
CTACACAGTC GGCTACAGCA CTTCCCTCGC CACCCTCACT ACTGCCATGG TCATCTTGTC	600
CCGCTTCCGG AAGCTGCATT GCACTCGCAA CTTTCATCCAC ATGAACCTGT TTGTATCCTT	660
CATGCTGAGG GCTATCTCCG TCTTCATCAA GGACTGGATC TTGTACGCCG AGCAGGACAG	720
CAGTCACTGC TTCGTTTCCA CCGTGGAGTG CAAAGCTGTC ATGGTTTTCT TCCACTACTG	780

CGTGGTGTCC	AACTACTTCT	GGCTGTTTCT	TGAAGGCCTG	TACCTCTTTA	CACTGCTGGT	840
GGAGACCTTC	TTCCCTGAGA	GGAGATATTT	CTACTGGTAC	ACCATCATCG	GCTGGGGGAC	900
ACCTACTGTG	TGTGTAACAG	TGTGGGCTGT	GCTGAGGCTC	TATTTTGATG	ATGCAGGATG	960
CTGGGATATG	AATGACAGCA	CAGCTCTGTG	GTGGGTGATC	AAAGGCCCCG	TGGTTGGCTC	1020
TATAATGGTT	AACTTTGTGC	TTTTTCATCG	CATCATCATC	ATCCTTGTAC	AGAAGCTGCA	1080
GTCCCCAGAC	ATGGGAGGCA	ACGAGTCCAG	CATCTACTTC	AGCTGCGTGC	AGAAATGCTA	1140
CTGCAAGCCA	CAGCGGGCTC	AGCAGCACTC	TTGCAAGATG	TCAGAACTAT	CCACCATTAC	1200
TCTACGGCTG	GCCCGCTCCA	CCCTACTGCT	CATCCCCTC	TTCGGAATCC	ACTACACAGT	1260
ATTGCGCTTC	TCTCCAGAGA	ACGTCAGCAA	GAGGGAAAGA	CTTGTGTTTG	AGCTTGGGCT	1320
GGGCTCCTTC	CAGGGCTTTG	TGGTGGCTGT	ACTCTACTGC	TTCCTGAATG	GGGAGGTACA	1380
GGCAGAGATT	AAGAGGAAAT	GGAGGAGCTG	GAAGGTGAAC	CGTTACTTCA	CTATGGACTT	1440
CAAGCACCGG	CACCCGTCCC	TGGCCAGCAG	TGGAGTAAAT	GGGGGAACCC	AGCTGTCCAT	1500
CCTGAGCAAG	AGCAGCTCCC	AGCTCCGCAT	GTCCAGCCTC	CCGGCCGACA	ACTTGGCCAC	1560
CTGAGGCCTG	TCTCCCTCCT	CCTTCTGCAC	AGGCTGGGGC	TGCGGGCCAG	TGCCTGAGCA	1620
TGTTTGTGCC	TCTCCCCTCT	CCTTGGGCAG	GCCCTGGGTA	GGAAGCTGGG	CTCCTCCCCA	1680
AAGGGGAAGA	GAGAGATAGG	GTATAGGCTG	ATATTGCTCC	TCCTGTTTGG	GTCCCACCTA	1740
CTGTGATTCA	TTGAGCCTGA	TTTGACATGT	AAATACACCT	CAAATTTGGA	AAGTTGCCCC	1800
ATCTCTGCCC	CCAACCCATG	CCCCTGCTCA	CCTCTGCCAG	GCCCCAGCTC	AACCTACTGT	1860
GTCAAGGCCA	GCCTCAGTGA	TAGTCTGATC	CCAGGTACAA	GGCCTTGTGA	GCTGAGGCTG	1920
AAAGGCCTGT	TTTGGAGAGG	CTGGGGTAGT	GCCCACCCCA	GCAGCCTTTC	AGCAAATTGA	1980
CTTTGGATGT	GGACCCTTCT	CAGCCTGTAC	CAAGTACTGC	AGTTGGCTAG	GGATGCAGCT	2040
CAGTTTCCTG	AGCATCCTTT	GGAGCAGGTC	AACCTGAGGC	TCCTTTTGCT	TACCCGACAT	2100
CTAAGTTGTC	CAGGTGCTCG	GCTCCTGTGT	GCCTGGATGA	CGGGAGGGCT	CCGGGGTCTT	2160
TCAGTCAAAG	ACTTACATTG	AGGTGGGGTG	AGAGTCAGAG	AAAAGTTCTG	GTGCTTTTCA	2220
TTTGTCTTAA	GAGCTGAGAG	CCAGGAATGC	AGAGTCAATT	GGGAAGGAGA	TGGGATAGCT	2280
GATGATCTTA	CCATGTCCAT	GACTGTGCCC	CTGATTCAAG	ACCGGATCAT	GTGGTGGCTT	2340

TATTTCTACA CTTCTTGTCC ACAATGGACA GTCTGAGGAA GCTCTTCTTT CAGCCACAAC	2400
AACCACAGAA AGCCCTTTCT TCTCCCCTCT TGTTCCTCCA TAAGTCAAAG CCATGTTTAG	2460
AACGGACCAG CCACCTTGCG ATGAAATCAC TGAGTTCTGA AGCAACTTTC AATTTCCACG	2520
AGCCAAGTCC TGGGTCCAGG GACGCCCC	2548

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 74..1648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCTG	120
TCCGTGGGGC CGGGGCAGAC TCCGCAAAGG ACGCGCAGCC TGCAAGTCCG CGGCCCAGAG	180
ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCAAGAAG	240
TGTCATGGCT GGTGTCGTGC ACGTTTCCCT GGCTGCTCTC CTCCTGCTGC CTATGGCCCC	300
TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCCTGG AGAAGATCCA	360
GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCCTCTCCA GGCTGTCCTG GGATGTGGGA	420
CAACATCACG TGTGGAAGC CCGCCCATGT GGGTGAGATG GTCCTGGTCA GCTGCCCTGA	480
GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCATTG GAGAGTCTGA	540
TTTTGGTGAC AGTAACTCCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC	600
GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTAATTTGAT GCCTGTGGGT TTGATGAATA	660
TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACACGGT	720
TGGCTACAGC ACATCCCTCG TCACCCTCAC CACTGCCATG GTCATCCTTT GTCGCTTCCG	780

GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTCGT TCATGCTGAG	840
GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG	900
CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTT TTCCACTACT GTGTTGTGTC	960
CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT	1020
CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGCTGGGGGT CCCCAACTGT	1080
GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT	1140
GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT	1200
TAACTTTGTG CTTTTTATTG GCATTATCGT CATCCTTGTG CAGAACTTC AGTCTCCAGA	1260
CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT	1320
CCCACTATTC GGAATCCACT ACACAGTATT TGCCTTCTCC CCAGAGAATG TCAGCAAAAG	1380
GGAAAGACTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCTTTGTGG TGGCTGTTCT	1440
CTACTGTTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAAATGGC GAAGCTGGAA	1500
GGTGAACCGT TACTTCGCTG TGGACTTCAA GCACCGACAC CCGTCTCTGG CCAGCAGTGG	1560
GGTGAATGGG GGCACCCAGC TCTCCATCCT GAGCAAGAGC AGCTCCCAA TCCGCATGTC	1620
TGGCCTCCCT GCTGACAATC TGGCCACCTG AGCCATGCTC CCCT	1664

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 74..1732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG	120

TCCGTGGGGC	CGGGGCAGAC	TCCGCAAAGG	ACGCGCAGCC	TGCAAGTCCG	CGGCCCAGAG	180
ACACATTGGG	GCTGACCTGC	CGCTGCTGTC	AGTGGGAGGC	CAGTGGTGCT	GGCCAAGAAG	240
TGTCATGGCT	GGTGTCTGTC	ACGTTTCCCT	GGCTGCTCTC	CTCCTGCTGC	CTATGGCCCC	300
TGCCATGCAT	TCTGACTGCA	TCTTCAAGAA	GGAGCAAGCC	ATGTGCCTGG	AGAAGATCCA	360
GAGGGCCAAT	GAGCTGATGG	GCTTCAATGA	TTCCTCTCCA	GGCTGTCTTG	GGATGTGGGA	420
CAACATCACG	TGTTGGAAGC	CCGCCCATGT	GGGTGAGATG	GTCCTGGTCA	GCTGCCCTGA	480
GCTCTTCCGA	ATCTTCAACC	CAGACCAAGT	CTGGGAGACC	GAAACCATTG	GAGAGTCTGA	540
TTTTGGTGAC	AGTAACTCCT	TAGATCTCTC	AGACATGGGA	GTGGTGAGCC	GGAAGTGCAC	600
GGAGGATGGC	TGGTCGGAAC	CCTTCCCTCA	TTACTTTGAT	GCCTGTGGGT	TTGATGAATA	660
TGAATCTGAG	ACTGGGGACC	AGGATTATTA	CTACCTGTCA	GTGAAGGCC	TCTACACGGT	720
TGGCTACAGC	ACATCCCTCG	TCACCCTCAC	CACTGCCATG	GTCATCCTTT	GTCGCTTCCG	780
GAAGCTGCAC	TGCACACGCA	ACTTCATCCA	CATGAACCTG	TTTGTGTCGT	TCATGCTGAG	840
GGCGATCTCC	GTCTTCATCA	AAGACTGGAT	TCTGTATGCG	GAGCAGGACA	GCAACCACTG	900
CTTCATCTCC	ACTGTGGAAT	GTAAGGCCGT	CATGGTTTTT	TTCCACTACT	GTGTTGTGTC	960
CATCTACTTC	TGGCTGTTCA	TCGAGGGCCT	GTACCTCTTC	ACTCTGCTGG	TGGAGACCTT	1020
CTTCCCTGAA	AGGAGATACT	TCTACTGGTA	CACCATCATT	GGCTGGGGGA	CCCCAACTGT	1080
GTGTGTGACA	GTGTGGGCTA	CGCTGAGACT	CTACTTTGAT	GACACAGGCT	GCTGGGATAT	1140
GAATGACAGC	ACAGCTCTGT	GGTGGGTGAT	CAAAGGCCCT	GTGGTTGGCT	CTATCATGGT	1200
TAACTTTGTG	CTTTTTTATTG	GCATTATCGT	CATCCTTGTG	CAGAACTTC	AGTCTCCAGA	1260
CATGGGAGGC	AATGAGTCCA	GCATCTACTT	CAGCTGCGTG	CAGAAATGCT	ACTGCAAGCC	1320
ACAGCGGGCT	CAGCAGCACT	CTTGCAAGAT	GTCAGAACTG	TCCACCATTA	CTCTGCGACT	1380
GGCCCCGTCC	ACCCTGCTGC	TCATCCCACT	ATTCGGAATC	CACTACACAG	TATTTGCCTT	1440
CTCCCCAGAG	AATGTCAGCA	AAAGGGAAAG	ACTCGTGTTT	GAGCTGGGGC	TGGGCTCCTT	1500
CCAGGGCTTT	GTGGTGGCTG	TTCTCTACTG	TTTTCTGAAT	GGTGAGGTAC	AAGCGGAGAT	1560
CAAGCGAAAA	TGGCGAAGCT	GGAAGGTGAA	CCGTTACTTC	GCTGTGGACT	TCAAGCACCG	1620
ACACCCGTCT	CTGGCCAGCA	GTGGGGTGAA	TGGGGGCACC	CAGCTCTCCA	TCCTGAGCAA	1680

GAGCAGCTCC CAAATCCGCA TGTCTGGCCT CCCTGCTGAC AATCTGGCCA CCTGAGCCAT 1740
GCTCCCCCT 1748

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1745 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 74..1729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG 60
GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG 120
TCCGTGGGGC CGGGGCAGAC TCCGCAAAGG ACGCGCAGCC TGCAAGTCCG CGGCCCAGAG 180
ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCAAGAAG 240
TGTGATGGCT GGTGTCGTGC ACGTTTCCCT GGCTGCTCTC CTCCTGCTGC CTATGGCCCC 300
TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCCTGG AGAAGATCCA 360
GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCCTCTCCA GGCTGTCCTG GGATGTGGGA 420
CAACATCACG TGTTGGAAGC CCGCCCATGT GGGTGAGATG GTCCTGGTCA GCTGCCCTGA 480
GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCATTG GAGAGTCTGA 540
TTTTGGTGAC AGTAACTCCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600
GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTAATTTGAT GCCTGTGGGT TTGATGAATA 660
TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACACGGT 720
TGGCTACAGC ACATCCCTCG TCACCCTCAC CACTGCCATG GTCATCCTTT GTCGCTTCCG 780
GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTCGT TCATGCTGAG 840
GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900

CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTTC TTCCACTACT GTGTTGTGTC	960
CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT	1020
CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGCTGGGGGA CCCCAACTGT	1080
GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT	1140
GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT	1200
TAACTTTGTG CTTTTTATTG GCATTATCGT CATCCTTGTG CAGAACTTC AGTCTCCAGA	1260
CATGGGAGGC AATGAGTCCA GCATCTACTT CTGCGTGCAG AAATGCTACT GCAAGCCACA	1320
GCGGGCTCAG CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TGCGACTGGC	1380
CCGCTCCACC CTGCTGCTCA TCCCCTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC	1440
CCCAGAGAAT GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA	1500
GGGCTTTGTG GTGGCTGTTT TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA	1560
GCGAAAATGG CGAAGCTGGA AGGTGAACCG TTA CTTCGCT GTGGACTTCA AGCACCGACA	1620
CCCGTCTCTG GCCAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG	1680
CAGCTCCCAA ATCCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACCT GAGCCATGCT	1740
CCCGT	1745

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 74..1732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG	120

TCCGTGGGGC	CGGGGCAGAC	TCCGCAAAGG	ACGCGCAGCC	TGCAAGTCCG	CGGCCCAGAG	180
ACACATTGGG	GCTGACCTGC	CGCTGCTGTC	AGTGGGAGGC	CAGTGGTGCT	GGCCAAGAAG	240
TGTCATGGCT	GGTGTCTGTC	ACGTTTCCCT	GGCTGCTCTC	CTCCTGCTGC	CTATGGCCCC	300
TGCCATGCAT	TCTGACTGCA	TCTTCAAGAA	GGAGCAAGCC	ATGTGCCTGG	AGAAGATCCA	360
GAGGGCCAAT	GAGCTGATGG	GCTTCAATGA	TTCCTCTCCA	GGCTGTCCTG	GGATGTGGGA	420
CAACATCACG	TGTTGGAAGC	CCGCCCATGT	GGGTGAGATG	GTCCTGGTCA	GCTGCCCTGA	480
GCTCTTCCGA	ATCTTCAACC	CAGACCAAGT	CTGGGAGACC	GAAACCATTG	GAGAGTCTGA	540
TTTTGGTGAC	AGTAACTCCT	TAGATCTCTC	AGACATGGGA	GTGGTGAGCC	GGAAGTGCAC	600
GGAGGATGGC	TGGTCGGAAC	CCTTCCCTCA	TTACTTTGAT	GCCTGTGGGT	TTGATGAATA	660
TGAATCTGAG	ACTGGGGACC	AGGATTATTA	CTACCTGTCA	GTGAAGGCCC	TCTACACGGT	720
TGGCTACAGC	ACATCCCTCG	TCACCCTCAC	CACTGCCATG	GTCATCCTTT	GTCGCTTCCG	780
GAAGCTGCAC	TGCACACGCA	ACTTCATCCA	CATGAACCTG	TTTGTGTCTG	TCATGCTGAG	840
GGGATCTCC	GTCTTCATCA	AAGACTGGAT	TCTGTATGCG	GAGCAGGACA	GCAACCACTG	900
CTTCATCTCC	ACTGTGGAAT	GTAAGGCCGT	CATGGTTTTT	TTCCACTACT	GTGTTGTGTC	960
CAACTACTTC	TGGCTGTTCA	TCGAGGGCCT	GTACCTCTTC	ACTCTGCTGG	TGGAGACCTT	1020
CTTCCTGAA	AGGAGATACT	TCTACTGGTA	CACCATCATT	GGCTGGGGGA	CCCCAACTGT	1080
GTGTGTGACA	GTGTGGGCTA	CGCTGAGACT	CTACTTTGAT	GACACAGGCT	GCTGGGATAT	1140
GAATGACAGC	ACAGCTCTGT	GGTGGGTGAT	CAAAGGCCCT	GTGGTTGGCT	CTATCATGGT	1200
TAACTTTGTG	CTTTTTATTG	GCATTATCGT	CATCCTTGTG	CAGAAACTTC	AGTCTCCAGA	1260
CATGGGAGGC	AATGAGTCCA	GCATCTACTT	AACAAATTTA	AGCCCGCGAG	TCCCCAAGAA	1320
AGCCCGAGAG	GACCCCCTGC	CTGTGCCCTC	AGACCAGCAT	TCACTCCCTT	TCCTGCGACT	1380
GGCCCGGTCC	ACCCTGCTGC	TCATCCCACT	ATTCGGAATC	CACTACACAG	TATTTGCCTT	1440
CTCCCCAGAG	AATGTCAGCA	AAAGGGAAAG	ACTCGTGTTT	GAGCTGGGGC	TGGGCTCCTT	1500
CCAGGGCTTT	GTGGTGGCTG	TTCTCTACTG	TTTTCTGAAT	GGTGAGGTAC	AAGCGGAGAT	1560
CAAGCGAAAA	TGGCGAAGCT	GGAAGGTGAA	CCGTTACTTC	GCTGTGGACT	TCAAGCACCG	1620
ACACCCGTCT	CTGGCCAGCA	GTGGGGTGAA	TGGGGGCACC	CAGCTCTCCA	TCCTGAGCAA	1680

GAGCAGCTCC CAAATCCGCA TGTCTGGCCT CCCTGCTGAC AATCTGGCCA CCTGAGCCAT 1740
GCTCCCCCT 1748

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln
1 5 10 15
Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu Gly Lys Arg Tyr Lys
20 25 30
Gln Arg Val Lys Asn Lys
35

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln
1 5 10 15
Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu
20 25

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGAAAGCTT CGGACCATGC GCCCTCCGAG CCCACCG

37

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCTCTAGA CGGTCAGACC AGGGAGACCT CCGCTTG

37

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGGATCTTCT CCAGGTGCAT DGCCTGCTCC TTCTTGAAGA TGTGGTC

47

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTGGGATATG AATGACAGCA CAGC

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCTGGGGAGA AGGCAAATAC TGTG

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TGCGTGCAGA AATGCTACTG CAAGCCACAG

30

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GACCCCCTGC CTGTGCCCTC AGACCAGCAT

30

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30